

GeneTools version 4.5
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nm protein - protein search, using sw model

Run on: February 28, 2002, 11:18:58 ; Search time 29.2 Seconds
(without alignments)
1200.010 Million cell updates/sec

File: us-09-576-778-10_copy_26_485
Port score: 25.25
Sequence: 1 ASADGTHHGGATLTKKSTL.....VAMGQPKKAYVQDDEP 460

Scoring table: BL/SM62
Gapop 10.0, Gapext 0.5

Starched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post processing: Minimum Hit: 09
Maximum Hit: 1000
Listing first 45 summaries

Database: 1: BL1:
2: BL2:
3: BL3:
4: BL4:

pred. No. is the number of results produced by others to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1817.5	72.0	553	2	140807
2	1817.5	72.0	553	2	cellulase (EC 3.2.1.4)
3	1469.5	58.2	879	2	endo-1,4-beta-glucanase I (E
4	1384.5	54.8	1045	2	endo-1,4-beta-glucanase B (E
5	1383.5	54.8	1711	2	thermo-1,4-beta-glucanase
6	1382.5	54.8	906	2	endo-beta-1,4-glu
7	1373.5	54.4	1742	2	cellulase (EC 3.2.1.4)
8	1354.5	53.6	739	2	cellulase (EC 3.2.1.4)
9	1354.5	53.6	739	2	cellulase (EC 3.2.1.4)
10	1213.5	43.2	705	2	endo-1,4-beta-glucanase
11	1074	41.5	1070	2	endo-1,4-beta-glucanase
12	1044	41.5	1070	2	endo-1,4-beta-glucanase
13	978	38.7	625	2	endo-1,4-beta-glucanase
14	971	38.7	625	2	endo-1,4-beta-glucanase
15	951.5	37.7	620	2	endo-1,4-beta-glucanase
16	943	37.7	620	2	endo-1,4-beta-glucanase
17	923	36.6	491	2	endo-1,4-beta-glucanase
18	908.5	35.9	491	2	endo-1,4-beta-glucanase
19	903	35.8	491	2	endo-1,4-beta-glucanase
20	900.5	35.7	490	2	endo-1,4-beta-glucanase
21	894.5	35.4	515	2	endo-1,4-beta-glucanase
22	889	35.2	515	2	endo-1,4-beta-glucanase
23	859	34.0	515	2	endo-1,4-beta-glucanase
24	852	33.7	479	2	endo-1,4-beta-glucanase
25	841.5	33.6	505	2	endo-1,4-beta-glucanase
26	844	33.4	510	2	endo-1,4-beta-glucanase
27	842	33.3	510	2	endo-1,4-beta-glucanase
28	842	33.3	510	2	endo-1,4-beta-glucanase
29	830.5	32.9	506	2	endo-1,4-beta-glucanase

1	828	42.8	507	2	S46500	cellulase (EC 3.2.1.4)
2	828	42.8	516	2	T01419	cellulase (EC 3.2.1.4)
3	826	42.7	506	2	T07226	endo-1,4-beta-g
4	824.5	42.6	501	2	T06348	cellulase (EC 3.2.1.4)
5	823	42.6	479	2	T07025	cellulase (EC 3.2.1.4)
6	821.5	42.5	496	2	T11783	cellulase (EC 3.2.1.4)
7	813.5	42.2	494	2	S11946	endo-1,4-beta-glu
8	807	42.0	501	2	A86158	cellulase (EC 3.2.1.4)
9	807	42.0	501	2	T52135	cellulase (EC 3.2.1.4)
10	793	41.4	488	2	T07885	cellulase (EC 3.2.1.4)
11	782	41.0	489	2	T06350	cellulase (EC 3.2.1.4)
12	781	40.9	621	2	S71215	endo-1,4-beta-glu
13	771	40.5	492	2	K96731	beta-glucanase I (E
14	768.5	40.4	484	2	C86362	cellulase (EC 3.2.1.4)
15	754	39.9	486	2	T06770	cellulase (EC 3.2.1.4)
16	748.5	39.6	489	2	E86466	protein F26F24.6 [

ALIGNMENTS

Result 1: 1
140807

cellulase (EC 3.2.1.4) cunc - Clostridium cellulovorans

Accession: F01419
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Size: 553
Date: 1996-08-28

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us-09-576-778-10_copy_26_485.rpr

Page 8

Search completed: February 28, 2002, 11:20:27
Jury Room: 409 Sosa

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11 N.W. 1997 (Ref. 45, last sequence update)
 12 15-JUL-1998 (Ref. 46, last annotation update)
 13 ENZYME: A01.1.1.16 (EC 3.2.1.4) (Title: 1,4 alpha-D-glucanase E 4)
 14 (Glycosylase 1) (Glycosylase 1)
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Only Match: 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
Best Javelin Similarity: 57.00% Prod. No. 4.40e-100
Matches: 2000 Observations: 622 Mismatches: 172 Totals: 172 Wins: 0

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[illegible]

Query Match: 42.5%; Score 1074; Len 1; Length 705;
 Best Local Similarity: 48.4%; Pred. No. 8, 46-78;
 Matches: 21%; conservative: 64; Mismatches: 141; Indels: 24; Gaps: 82

145. WERNER, W. 1970. THE EFFECT OF TEMPERATURE ON THE GROWTH OF THE COMMON CARP (*Cyprinus carpio* L.) IN THE RIVER DANUBE. *Acta Zool. Bot. Hungarica* 16: 1-10.

[illegible][illegible]

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RESULT 10
CON_FLOW
10 CON_FLOW
STATE: 0
PRT 40 AA

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the classification of $\mathcal{A}(\mathcal{A})$ in the class of \mathcal{A} -modules.

1. S. H. CRANE, *et al.*, *Proc. Nat. Acad. Sci. U.S.A.*, **45**, 102 (1954).

ET, regulation of stress expression by ethylene and auxin";
55. "Plant Physiol. 66:1257-1264 (1980).
56. "FURTHER EVIDENCE IN RELATION TO FRUIT RESIST-
60. "CATALYTICALLY ACTIVE ENDOHYDROLASES OF 1,4-BE-
LINKAGES IN CELLULOSE."
77.

DEVELOPMENTAL STAGE IN RETURNING FOLLOWS SIMILARITY BETWEEN THE CELLULOSE FAMILY AND HYDROLASES.

between the Swiss Institute of Microfilmatics and the Federal Statistical Office of the Swiss National Bank. There are no restrictions on its use by non-profit institutions as long as its content is in no way disclosed and that statements are not allowed, except by, and for, members of the Board of Directors.

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[illegible]

11	7.0% SILE	476	476	BY CONTINUITY
12	COEFFICIENT	460	466	INSUREN - 2.101110 (IN REL. %)
13	RECOGNICE	426 AA	544-1	ME: 673605BP5767640 (10364)

Event: Match	42, 58;	Score 821-57;	146 1;	Length 499;
Post: Local Similarity	36, 88;	Prod. No. 6;	Ch 5H;	
Match: 11;	Consecutive 85;	Mismatches 170;	Indels 49;	Others 7;

107 1.26 HAWORTH, H. R. A. and THORNTON, A. A. A. *Aspects of Protein Synthesis*. 1967

01 247 ERYTHRO-AMINO ACID TRANSFERASE (EC 2.3.1.30) FROM *STREPTOCOCCUS*
 02 *FAECIUM* (ATCC 29521) (1979) 111-113
 03 04 273 OXALATES -- EPIMERIZATION TO D-GLUCARATE BY AERIAL BACTERIA (1979) 127
 05 06 406 11773 11774 11775 11776 11777 11778 11779 11780 11781 11782 11783 11784 11785 11786 11787 11788 11789 11790 11791 11792 11793 11794 11795 11796 11797 11798 11799 11800 11801 11802 11803 11804 11805 11806 11807 11808 11809 11810 11811 11812 11813 11814 11815 11816 11817 11818 11819 11820 11821 11822 11823 11824 11825 11826 11827 11828 11829 11830 11831 11832 11833 11834 11835 11836 11837 11838 11839 11840 11841 11842 11843 11844 11845 11846 11847 11848 11849 11850 11851 11852 11853 11854 11855 11856 11857 11858 11859 11860 11861 11862 11863 11864 11865 11866 11867 11868 11869 11870 11871 11872 11873 11874 11875 11876 11877 11878 11879 11880 11881 11882 11883 11884 11885 11886 11887 11888 11889 11890 11891 11892 11893 11894 11895 11896 11897 11898 11899 11900 11901 11902 11903 11904 11905 11906 11907 11908 11909 11910 11911 11912 11913 11914 11915 11916 11917 11918 11919 11920 11921 11922 11923 11924 11925 11926 11927 11928 11929 11930 11931 11932 11933 11934 11935 11936 11937 11938 11939 11940 11941 11942 11943 11944 11945 11946 11947 11948 11949 11950 11951 11952 11953 11954 11955 11956 11957 11958 11959 11960 11961 11962 11963 11964 11965 11966 11967 11968 11969 11970 11971 11972 11973 11974 11975 11976 11977 11978 11979 11980 11981 11982 11983 11984 11985 11986 11987 11988 11989 11990 11991 11992 11993 11994 11995 11996 11997 11998 11999 12000 12001 12002 12003 12004 12005 12006 12007 12008 12009 12010 12011 12012 12013 12014 12015 12016 12017 12018 12019 12020 12021 12022 12023 12024 12025 12026 12027 12028 12029 12030 12031 12032 12033 12034 12035 12036 12037 12038 12039 12040 12041 12042 12043 12044 12045 12046 12047 12048 12049 12050 12051 12052 12053 12054 12055 12056 12057 12058 12059 12060 12061 12062 12063 12064 12065 12066 12067 12068 12069 12070 12071 12072 12073 12074 12075 12076 12077 12078 12079 12080 12081 12082 12083 12084 12085 12086 12087 12088 12089 12090 12091 12092 12093 12094 12095 12096 12097 12098 12099 12100 12101 12102 12103 12104 12105 12106 12107 12108 12109 12110 12111 12112 12113 12114 12115 12116 12117 12118 12119 12120 12121 12122 12123 12124 12125 12126 12127 12128 12129 12130 12131 12132 12133 12134 12135 12136 12137 12138 12139 12140 12141 12142 12143 12144 12145 12146 12147 12148 12149 12150 12151 12152 12153 12154 12155 12156 12157 12158 12159 12160 12161 12162 12163 12164 12165 12166 12167 12168 12169 12170 12171 12172 12173 12174 12175 12176 12177 12178 12179 12180 12181 12182 12183 12184 12185 12186 12187 12188 12189 12190 12191 12192 12193 12194 12195 12196 12197 12198 12199 12200 12201 12202 12203 12204 12205 12206 12207 12208 12209 12210 12211 12212 12213 12214 12215 12216 12217 12218 12219 12220 12221 12222 12223 12224 12225 12226 12227 12228 12229 12230 12231 12232 12233 12234 12235 12236 12237 12238 12239 12240 12241 12242 12243 12244 12245 12246 12247 12248 12249 12250 12251 12252 12253 12254 12255 12256 12257 12258 12259 12260 12261 12262 12263 12264 12265 12266 12267 12268 12269 12270 12271 12272 12273 12274 12275 12276 12277 12278 12279 12280 12281 12282 12283 12284 12285 12286 12287 12288 12289 12290 12291 12292 12293 12294 12295 12296 12297 12298 12299 12300 12301 12302 12303 12304 12305 12306 12307 12308 12309 12310 12311 12312 12313 12314 12315 12316 12317 12318 12319 12320 12321 12322 12323 12324 12325 12326 12327 12328 12329 12330 12331 12332 12333 12334 12335 12336 12337 12338 12339 12340 12341 12342 12343 12344 12345 12346 12347 12348 12349 12350 12351 12352 12353 12354 12355 12356 12357 12358 12359 12360 12361 12362 12363 12364 12365 12366 12367 12368 12369 12370 12371 12372 12373 12374 12375 12376 12377 12378 12379 12380 12381 12382 12383 12384 12385 12386 12387 12388 12389 12390 12391 12392 12393 12394 12395 12396 12397 12398 12399 12400 12401 12402 12403 12404 12405 12406 12407 12408 12409 12410 12411 12412 12413 12414 12415 12416 12417 12418 12419 12420 12421 12422 12423 12424 12425 12426 12427 12428 12429 1243

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 02 02/271,983
3 FILING DATE: 07-JUL-1994
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 02 02/087,466
6 FILING DATE: 16-APR-1991
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 92 03/7511,417
9 FILING DATE: 20-APR-1990
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Bastian, Kevin L.
12 PRACTICING ADDRESS: 41721
13 REFERENCE/SEQUENCE NUMBER: 02/071,304/300S
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (415) 548-0600
16 TELEFAX: (415) 548-0438
17 INTERNATIONAL FILING: 2
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 501 amino acids
20 TYPE: amino acid
21 TOPOLOGY: linear
22 MOLECULE TYPE: protein
23 OS-08-434-702-2

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Every Match	32.68	Score	824.5	18.1	Length	501			
Best Total	30.19	Prod	650.76						
Matches	181	Conservative	79	Mismatches	169	Indels	47	Caps	10

[illegible]

NUMBER OF STUDENTS: 10
ACADEMIC ADDRESS:
ADDRESSEE: Townsend and Townsend Knottle and O'Neil
STREET: Steadth Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1194
REPORT AVAILABLE FROM:
RELATION TYPE: Pl-997 disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Potch to Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTENTION NUMBER: 07/08/271.883
FILING DATE: 07-JUL-1994
CLASSIFICATION: 445
APPLICATION NUMBER: 05 07/087.466
FILING DATE: 18-APR-1991
ERROR APPLICATION DATA:
APPLICATION NUMBER: 05 07/511.417
FILING DATE: 20-APR-1990
ALTERNATIVE/AGENT INFORMATION:
NAME: Bastien, Kevin L.
REGISTRATION NUMBER: 34.774
ENTERED BY: YES NUMBER: 2407E-004-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 544-5000
TELEFAX: (415) 544-5043
INFORMATION FOR CRO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
FUNCTION: linear
FAMILY: Proteoin
US-08 471 883 2

5000; depth 22.6 m; score 823.5; DB 1; length 50);

[illegible]

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 FR 21-MAY-1999 900S-0132151.
 FR 24-MAY-1999 900S-0145627.
 FR 25-MAY-1999 900S-0146021.
 FR 27-MAY-1999 900S-0146492.
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Database: us-09-576-778-10_copy_26_646.rsp
 Sequence: 1

Result: 1

Score: 100.0, Expect: 0.0

Database: 1

Sequence: 1

Score: 100.0, Expect: 0.0

Database: 1

Sequence: 1

Score: 100.0, Expect: 0.0

Database: 1

Sequence: 1

Score: 100.0, Expect: 0.0

Database: 1

Sequence: 1

Score: 100.0, Expect: 0.0

SUMMARY

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Expect	Database	Sequence
1	2304.5	68.1	1	1
2	1967.5	57.9	1	1
3	1864.5	55.1	1	1
4	1809.5	53.5	1	1
5	1748.5	51.7	1	1
6	1747.5	51.7	1	1
7	1727.5	51.1	1	1
8	1674.5	49.9	1	1
9	1624.5	48.4	1	1
10	1621.5	48.4	1	1
11	1614.5	48.1	1	1
12	1600.5	47.1	1	1
13	1587.5	46.2	1	1
14	1587.5	46.2	1	1
15	1587.5	46.2	1	1
16	1587.5	46.2	1	1
17	1587.5	46.2	1	1
18	1587.5	46.2	1	1
19	1587.5	46.2	1	1
20	1587.5	46.2	1	1
21	1587.5	46.2	1	1
22	1587.5	46.2	1	1
23	1587.5	46.2	1	1
24	1587.5	46.2	1	1
25	1587.5	46.2	1	1
26	1587.5	46.2	1	1
27	1587.5	46.2	1	1
28	1587.5	46.2	1	1
29	1587.5	46.2	1	1
30	1587.5	46.2	1	1
31	1587.5	46.2	1	1
32	1587.5	46.2	1	1
33	1587.5	46.2	1	1

Result No.	Score	Expect	Database	Sequence	Accession
1	2304.5	68.1	1	1	U00000
2	1967.5	57.9	1	1	U00000
3	1864.5	55.1	1	1	U00000
4	1809.5	53.5	1	1	U00000
5	1748.5	51.7	1	1	U00000
6	1747.5	51.7	1	1	U00000
7	1727.5	51.1	1	1	U00000
8	1674.5	49.9	1	1	U00000
9	1624.5	48.4	1	1	U00000
10	1621.5	48.4	1	1	U00000
11	1614.5	48.1	1	1	U00000
12	1600.5	47.1	1	1	U00000
13	1587.5	46.2	1	1	U00000
14	1587.5	46.2	1	1	U00000
15	1587.5	46.2	1	1	U00000
16	1587.5	46.2	1	1	U00000
17	1587.5	46.2	1	1	U00000
18	1587.5	46.2	1	1	U00000
19	1587.5	46.2	1	1	U00000
20	1587.5	46.2	1	1	U00000
21	1587.5	46.2	1	1	U00000
22	1587.5	46.2	1	1	U00000
23	1587.5	46.2	1	1	U00000
24	1587.5	46.2	1	1	U00000
25	1587.5	46.2	1	1	U00000
26	1587.5	46.2	1	1	U00000
27	1587.5	46.2	1	1	U00000
28	1587.5	46.2	1	1	U00000
29	1587.5	46.2	1	1	U00000
30	1587.5	46.2	1	1	U00000
31	1587.5	46.2	1	1	U00000
32	1587.5	46.2	1	1	U00000
33	1587.5	46.2	1	1	U00000

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RESULTS

[illegible][illegible]

No.	NAME	AGE	RELATION	RELATIVE STABILITY
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6	6	99	6	100
7	7	100	7	100
8	8	101	8	100
9	9	102	9	100
10	10	103	10	100
11	11	104	11	100
12	12	105	12	100
13	13	106	13	100
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15	15	108	15	100
16	16	109	16	100
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20	20	113	20	100
21	21	114	21	100
22	22	115	22	100
23	23	116	23	100
24	24	117	24	100
25	25	118	25	100
26	26	119	26	100
27	27	120	27	100
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32	32	125	32	100
33	33	126	33	100
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40	40	133	40	100
41	41	134	41	100
42	42	135	42	100
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78	78	171	78	100
79	79	172	79	100
80	80	173	80	100
81	81	174	81	100
82	82	175	82	100
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Host Local Similarity	50, 38	Prod. No.	2, 6	127		
Model No.	257	Consistency	1507	Models	207	Stars
						107

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[illegible][illegible]



[illegible][illegible]

[illegible]

Accession	Gene	Species	Length (aa)	Accession	Gene	Species	Length (aa)
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26	219	101FPA01	110	26	219	101FPA01	110
27	217	EMED2201	100	27	217	EMED2201	100
28	275	FW	100	28	275	FW	100
29	307	Y17030	100	29	307	Y17030	100
30	304	Y17030	100	30	304	Y17030	100
31	304	Y17030	100	31	304	Y17030	100
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Idb 1927 TREVINO 1982

RESULT 5

REF ID: A146014

LOCUS: A146014

ACCESSION: A146014

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 KW Protein identification: signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
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 XX Arabidopsis thaliana.
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 XX 06 SEP 2000.
 XX
 XX 25 FEB 2000; 2000EP-0301459.
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RESULT 14

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AC20815;

AC20815 (first entry)

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57 scattered, increases solid content, sugar content and acidity of fruit.
 58 the DNA can also be used for the construction of hybridisation probes
 59 and PCR primers to detect RNA and DNA encoding capsid proteinase.
 60
 61 Sequence 2504 bp; 742 A; 417 C; 895 G; 700 T; 0 other:

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 File: 110014006.seq

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 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7402
 Fax: 580 221 7400
 Email: radix@noble.org
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 Seq primer: 012 row: A column: 11
 Seq primer: TCACAGAGAAACAGTAAAGAC

BASE COUNT 145 a 142 c 140 g 139 t
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 Matches 4209 Conserved 07 Mismatches 2278 Indels 49 Gaps 11

TITLE

Expressed Sequence Tags from The Samuel Roberts Noble Foundation Medicago truncatula stem library

JOURNAL

Medicago truncatula stem library (unpublished) (2000)
 Character: 1,200 bp
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7402
 Fax: 580 221 7400
 Email: radix@noble.org
 Insert length: 683
 Seq primer: 012 row: A column: 11
 Seq primer: TCACAGAGAAACAGTAAAGAC

GENE

Medicago truncatula stem library (unpublished) (2000)

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USDA
National Center for Genetic Resource Preservation

Department of Botany

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Plant Sciences Building, Box 25-2, Athens, GA 30602-7271, USA

Phone: 706 542-1000

Fax: 706 542-1005

Email: amput@arches.uga.edu

Sequences have been trimmed to overlap polyA, vector, and regions

look three primers. The threshold for high quality sequence is

20. Those for the sequences, which are obtained with primers or 17

sequence primers, are presented as the reverse complement.

See primer: JEN REV

High quality sequence stop: 579

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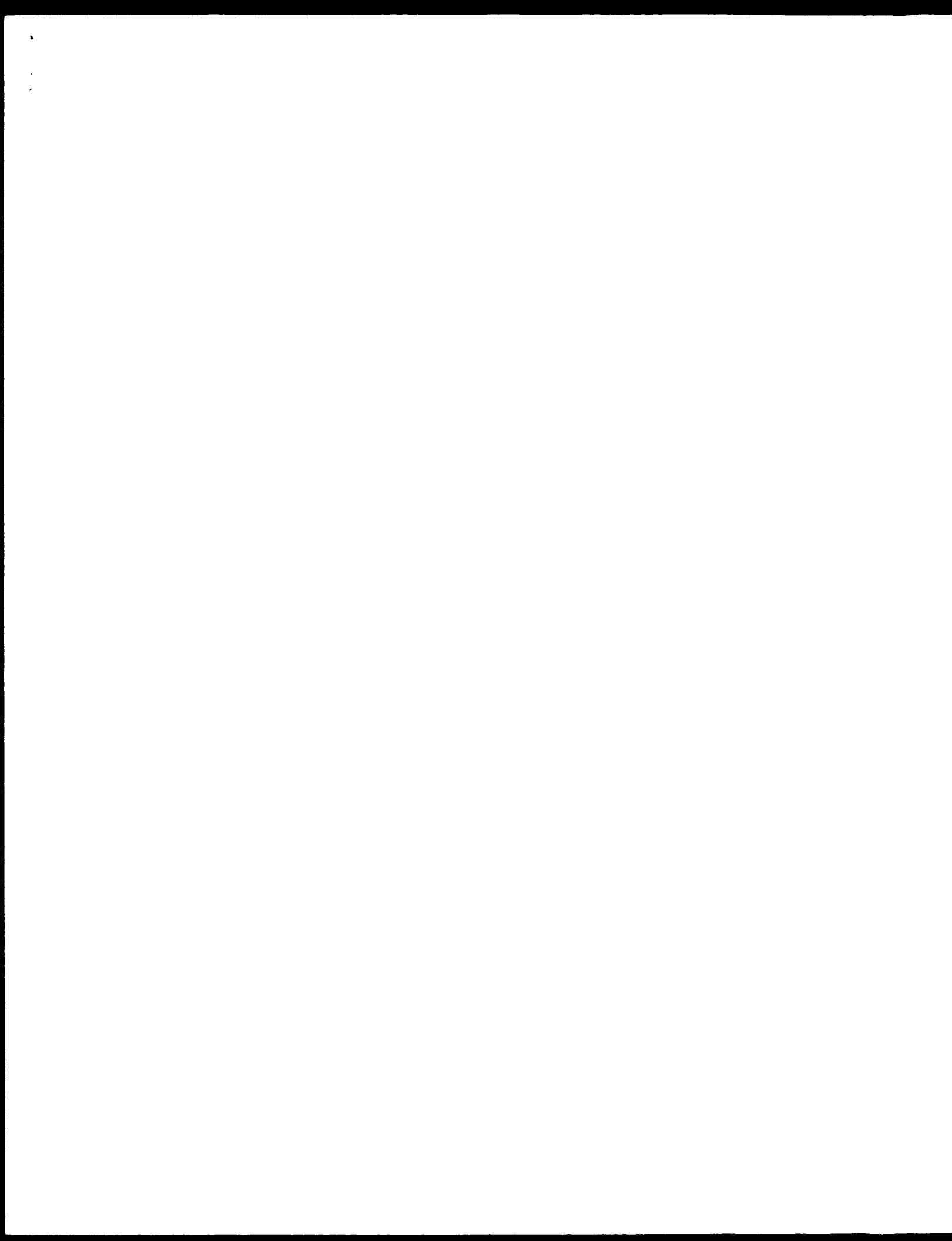
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10 508 gcttgcacacacacacacacacacacacacacacacacacacacacacacacacacac 567
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 568 aaatggttcttataagatcaatgagcggatgtcggggttaagacattgttgatgataa 609
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Search completed: February 28, 2002, 22:59:55
 Job time: 4937 sec



GenScan version 4.5
Copyright (c) 1994 - 2000 Campbell Ltd.

us protein - protein search, using ss model

Run on: February 28, 2002, 11:18:58 Search Time 11.02 Seconds

(without alignment)

762,041 hits in 0.11 of 345,000,000

US-09-576-778-10_Protein.usc.usc

Percent score: 26.25

us-09-576-778-10_Protein.usc.usc

Search table:

MaxScore: 10.0, GapPen: 0.5

Search: 522463 seqs, 74073290 positions

Total number of hits satisfying chosen parameters: 522463

Minimum E-value: 0

Maximum hit seq length: 200000000

Post-processing: Minimum March 08

Maximum March 10/98

Listing first 45 summaries

Database:

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SUMMARIES

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Prod. No.	Match	Match Length	DB	DB	Prod. No.
1	25.25	100.0	64.9	22	AA06066	Basillus thuringiensis	1
2	17.65	70.1	64.9	15	AA14709	Cellulase ABC	2
3	14.02	51.6	17.1	20	AA11844	Truncated cellulase	3
4	11.42	45.2	8.75	19	AA01907	Basillus thuringiensis	4
5	10.76	42.6	4.18	20	AA02146	Cellulase ABC	5
6	10.11	40.9	4.46	20	AA02146	Cellulase ABC	6
7	8.94	45.4	5.25	21	AA02146	Cellulase ABC	7
8	8.89	45.2	5.25	21	AA02146	Cellulase ABC	8
9	8.84	45.0	7.54	21	AA02146	Cellulase ABC	9
10	8.52	44.7	4.68	21	AA02146	Cellulase ABC	10
11	8.52	44.7	4.72	21	AA02146	Cellulase ABC	11

Prod. No.	Score	Prod. No.	Match	Match Length	DB	DB	Prod. No.
12	8.52	44.7	4.72	21	AA02146	Cellulase ABC	12
13	8.48	44.2	4.73	21	AA02146	Cellulase ABC	13
14	8.48	44.2	4.73	21	AA02146	Cellulase ABC	14
15	8.48	44.2	4.73	21	AA02146	Cellulase ABC	15
16	8.48	44.2	4.73	21	AA02146	Cellulase ABC	16
17	8.48	44.2	4.73	21	AA02146	Cellulase ABC	17
18	8.48	44.2	4.73	21	AA02146	Cellulase ABC	18
19	8.48	44.2	4.73	21	AA02146	Cellulase ABC	19
20	8.48	44.2	4.73	21	AA02146	Cellulase ABC	20
21	8.48	44.2	4.73	21	AA02146	Cellulase ABC	21
22	8.48	44.2	4.73	21	AA02146	Cellulase ABC	22
23	8.48	44.2	4.73	21	AA02146	Cellulase ABC	23
24	8.48	44.2	4.73	21	AA02146	Cellulase ABC	24
25	8.48	44.2	4.73	21	AA02146	Cellulase ABC	25
26	8.48	44.2	4.73	21	AA02146	Cellulase ABC	26
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41	8.48	44.2	4.73	21	AA02146	Cellulase ABC	41
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43	8.48	44.2	4.73	21	AA02146	Cellulase ABC	43
44	8.48	44.2	4.73	21	AA02146	Cellulase ABC	44
45	8.48	44.2	4.73	21	AA02146	Cellulase ABC	45

REFERENCES

Prod. No.	Score	Prod. No.	Match	Match Length	DB	DB	Prod. No.
1	25.25	100.0	64.9	22	AA06066	Basillus thuringiensis	1
2	17.65	70.1	64.9	15	AA14709	Cellulase ABC	2
3	14.02	51.6	17.1	20	AA11844	Truncated cellulase	3
4	11.42	45.2	8.75	19	AA01907	Basillus thuringiensis	4
5	10.76	42.6	4.18	20	AA02146	Cellulase ABC	5
6	10.11	40.9	4.46	20	AA02146	Cellulase ABC	6
7	8.94	45.4	5.25	21	AA02146	Cellulase ABC	7
8	8.89	45.2	5.25	21	AA02146	Cellulase ABC	8
9	8.84	45.0	7.54	21	AA02146	Cellulase ABC	9
10	8.52	44.7	4.68	21	AA02146	Cellulase ABC	10
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XX      03- AUG- 1999: 9908- 0147204.
XX      04- AUG- 1999: 9908- 0147302.
XX      05- AUG- 1999: 9908- 0147192.
XX      05- AUG- 1999: 9908- 0147260.
XX      06- AUG- 1999: 9908- 0147303.
XX      06- AUG- 1999: 9908- 0147416.
XX      09- AUG- 1999: 9908- 0147943.
XX      09- AUG- 1999: 9908- 0147945.
XX      10- AUG- 1999: 9908- 0148171.
XX      11- AUG- 1999: 9908- 0148316.
XX      12- AUG- 1999: 9908- 0148341.
XX      13- AUG- 1999: 9908- 0148565.
XX      13- AUG- 1999: 9908- 0148684.
XX      16- AUG- 1999: 9908- 0149368.
XX      17- AUG- 1999: 9908- 0149375.
XX      18- AUG- 1999: 9908- 0149426.
XX      20- AUG- 1999: 9908- 0149722.
XX      20- AUG- 1999: 9908- 0149723.
XX      20- AUG- 1999: 9908- 0149929.
XX      23- AUG- 1999: 9908- 0149902.
XX      23- AUG- 1999: 9908- 0149940.
XX      25- AUG- 1999: 9908- 0150566.
XX      26- AUG- 1999: 9908- 0150884.
XX      27- AUG- 1999: 9908- 0151065.
XX      27- AUG- 1999: 9908- 0151066.
XX      27- AUG- 1999: 9908- 0151080.
XX      30- AUG- 1999: 9908- 0151303.
XX      31- AUG- 1999: 9908- 0151438.
XX      01- SEP- 1999: 9908- 0151940.
XX      01- SEP- 1999: 9908- 0152363.
XX      10- SEP- 1999: 9908- 0153070.
XX      13- SEP- 1999: 9908- 0153758.
XX      17- SEP- 1999: 9908- 0154018.

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